AMENDMENTS TO THE CLAIMS, COMPLETE LISTING OF CLAIMS IN ASCENDING ORDER WITH STATUS INDICATOR

1. (Currently Amended) A method of detecting mutation in ~~the~~a base sequence of nucleic acid, including:

(A) a bonding step of hybridizing an object of analysis~~, consisting of nucleic acid or a nucleic acid fragment including a plurality of inspected sites to be subjected to inspection of mutation in the base sequence,~~ with a plurality of labeled oligonucleotides of varying types, said object of analysis (1) consisting of nucleic acid or a nucleic acid fragment having a base sequence and (2) including a plurality of inspected sites in the base sequence to be subjected to inspection of mutation, each oligonucleotide having a base sequence that is complementary to at least one normal base sequence of one of the inspected sites, and each oligonucleotide being labeled to be discriminable from each other for forming duplexes including hetero- and homoduplexes; and

(B) a detection step for detecting said mutation, which can be located at any position throughout the base sequence of said object of analysis, by employing an ion pair chromatograph comprising a reversed phase column serving as a separation column and a detector capable of discriminating and detecting the labeled oligonucleotides, and setting the separation column at a temperature at which there is a difference in stability between the hetero- and homoduplexes included in the duplexes for analyzing the object of analysis.

2. (Currently Amended) The mutation detecting method according to claim 1, wherein the oligonucleotides are labeled with ~~the~~ fluorescent materials.

3. (Currently Amended) The mutation detecting method according to claim 1, wherein the separation column is set at ~~the~~a melting temperature of the heteroduplex.

4. (Previously Presented) The mutation detecting method according to claim 1, which further comprises observing a chromatogram of labels obtained through the detection step (B), and thereby determining that an inspected site corresponding to a label is non-mutational due to the presence of a single peak, while further determining that an inspected site corresponding to a label is mutational due to the presence of two peaks.

5. (Original) The mutation detecting method according to claim 1, including an amplification step of amplifying the object of analysis in advance of the bonding step (A).

6. (Currently Amended) The mutation detecting method according to claim 5, wherein the amplification step is a single PCR ~~step~~ cycle.